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SEQ ID NO: 6	A33	1	W V G K W W P V L W T L C A V R V T Y D A I S V E T P Q D V L R A S Q G K S V T L P C T Y H T S T S
SEQ ID NO: 1	40628	1	W G T K A Q V E R K L C F I L A I L C S L A L G S V T V H S S E . . . . . P E V A I P E
SEQ ID NO: 2	45416	1	... W G I L L G L L L G H L T Y D I Y G R P I L E V P E S V T G P W K G D V N I L P C T Y D P L
SEQ ID NO: 9	35638	1	W A R R S R H R L L L L L R Y L V V A L G Y H K A Y G F S A P K D Q . . . . . Q V V T A V E
SEQ ID NO: 10	JAM	1	W G T E G K A G R K L L F L F T S M I L G S L V Q G K G S V Y T A Q . . . . . S D V Q V P E
A33	51	S R E G L I Q W O K L L L T E R V V I W P F S H N K N Y I H G E L Y K N R V S I S H N A E Q S D A	
40628	43	N N P V K L S C A Y S G F S S P R V E W K F D Q G D T T R L Y C Y N N K I T A S Y E D R V T F L P T	
45416	47	Q G Y T Q V L Y K W L V Q R G S D P V T I F L R D S S G D H I Q Q A K Y Q G R L H V S H K V P G O V	
35638	43	Y Q E A I L A C K T P K X T V S S R L E W K K L G R S V S F Y Y Q Q T L Q G D F K H R A E M I D F	
JAM	42	N E S I K L T C T Y S G F S S P R V E W K F V Q G S T T A L Y C Y N S Q I T A P Y A D R V T F S S S	
A33	101	S I T I D Q L T I A D N G T Y E C S V S L . . . . . S D L E G N T K S V A Y R L V L V P P S K	
40628	93	G I T F K S V T R E D T G T Y T C H V S E . . . . . E G G N S Y G E V K Y K L I V L V P P S K	
45416	97	S I Q L S T L E W D D O R S H Y T C E V T W O T P D G N O V V R D K I T E L R V Q K L S V S K P T V T	
35638	93	N I R I K N V T R S D A G K Y R C E V S A P S . . . . . E O G G N L E E D T Y T L E V L V A P A V	
JAM	92	G I T F S S V T R K D N G E Y T C H V S E . . . . . E G G Q N Y G E V S I H L T V L V P P S K	
A33	144	P E C G I E G E T I I G N N I O L T C Q S K E G S P T P O Y S W K R Y N I L N Q E O . . . . .	
40628	135	P T V N I P S S A T I G N R A V L T C S E Q D G S P P S E Y T W F K D G I V W M P T N . P K S T R A F	
45416	147	T G S G Y G F T V P Q G M R I S L Q C O A R . G S P P I S Y I W Y Q Q T N N Q E P . . . . .	
35638	137	P S C E V P S S A L S G T V V E L R C Q D K E G N P A P E Y T W F K D G I R L L E N . P R L G S Q S	
JAM	134	P T I S V P S S V T I G N R A V L T C S E H D G S P P S E Y S W F K D G I S W L T A D A K K T R A F	

SEQ ID NO: 6	A33	186	... PLAQPASGQPVSLLKNISTDTSGYYICITSNEEG...	T OF C N I T V
SEQ ID NO: 1	40628	184	SNSSYVLNKPTTGELVFDP	TPMTSNAY
SEQ ID NO: 2	45416	188	... IKVATLSTLLFKP	TPMTSNAY
SEQ ID NO: 9	35638	186	TNSSYTWNTKTGTLQFNTVSKLDTGEYSCEARNSYG...	TPMTSNAY
SEQ ID NO: 10	JAM	184	WNSSSFTIDPKSGDLIFDOPVTAFDSGEYYCOKAQ...	TPMTSNAY

FIG. 1B

SEQ ID NO:1

Met	Gly	Thr	Lys	Ala	Gln	Val	Glu	Arg	Lys	Leu	Leu	Cys	Leu	Phe	Ile	Leu	Ala	Ile	Leu	Cys	Ser	Leu	Ala	Leu	Gly	Ser	Val	Thr																																
1	5	10	15	20	25	30	35	40	45	50	55	60	65	70	75	80	85	90	95	100	105	110	115	120	125	130	135	140	145	150	155	160	165	170	175	180	185	190	195	200	205	210	215	220	225	230	235	240	245	250	255	260	265	270	275	280	285	290	295	299

Val

His

Ser

Ser

Glu

Pro

Glu

Val

Arg

Ile

Pro

Glu

Asn

Asn

Pro

Val

Lys

Leu

Ser

Cys

Ala

Tyr

Ser

Gly

Phe

Ser

Ser

Pro

Arg

Val

65

70

75

80

85

90

95

100

105

110

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125

130

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FIG.\_2

SEQ ID NO:2

1 **MGILIGLIL** GHLIVDTYGR FILEVPESVT GPWKGDVNLP CTYDPLQGTYT QVLVKWLVQR GSDPVTIFLR DSSGDHICQA KYQGRLLHVSQH KVPGDVSIQL101 **STLEMDDRSH** YTCEVTWQTP DGNQVYRDKI TELRVQKLSV **SKPTVTTGSG** **YCFTVPGM** **ISLQCQARG** **PPISYI**WYKQ **QTNNQEPIKV** **ATLSTLJLFKP**  
~Glycosaminoglycan attachment site201 **AVIADSGSYF** CTAKGQVGSE QHSDIVKFVV KDSSKLKKTK TEAPTTMVTYP LKATSTVKQS WDWTTDMGY **LGETSAGPK** **SLPVFAILLI** **ISLCCMIVFT**  
~Transmembrane domain301 **MAYIMLCKT** SQQEHVYEEA ROLI2162 (35936.f1)  
SEQ ID NO:12

TCGCGGAGCTGTGTTCTGTTTCCC

OLI2163 (35936.p1)  
SEQ ID NO:13

TGATCGCGATGGGGACAAAGGCCAAGCTCGAGAGGAAACTGTTGTGCCT

OLI2164 (35936.f2)  
SEQ ID NO:14

ACACCTGGTTCAAAAGATGGG

OLI2165 (35936.r1)  
SEQ ID NO:15

TAGGAAGAGTTGCTGAAGGCACGG

**FIG.-3**OLI2166 (35936.f3)  
SEQ ID NO:16

TTGCCTTACTCAGGTCGCTAC

OLI2167 (35936.r2)  
SEQ ID NO:17

ACTCAGCAGTGGTAGGAAAG

**FIG.-8**

DNA35936 SEQ ID NO:3

CTTCTTGCCTA ACTGGTATCA CCTTCAAGTC CGTGACACGG GAAGACACTG 50  
 GGACATACAC TTGTATGGTC TCTGAGGAAG GCGGCAACAG CTATGGGGAG 100  
 GTCAAGGTCA AGCTCATCGT GCTTGTGCCT CCATCCAAGC CTACAGTTAA 150  
 CATCCCCTCC TCTGCCACCA TTGGGAACCG GGCAGTGCTG ACATGCTCAG 200  
 AACAAAGATGG TTCCCCACCT TCTGAATACA CCTGGTTCAA AGATGGGATA 250  
 GTGATGCCTA CGAATCCCAA AAGCACCCGT GCCTTCAGCA ACTCTTCCTA 300  
 TGTCCCTGAAT CCCACAAACAG GAGAGCTGGT CTTTGATCCC CTGTCAGCCT 350  
 CTGATACTGG AGAATACAGC TGTGAGGCAC GGAATGGGTA 390

**FIG.\_4A**

consen01 SEQ ID NO:4

TCTCAGTCCC CTCGCTGTAG TCGCGGAGCT GTGTTCTGTT TCCCAGGAGT 50  
 CCTTCGGCGG CTGTTGTGCT CAGGTGCGCC TGATCGCGAT GGGGACAAAG 100  
 GCGCAAGCTC GAGAGGAAAC TGTTGTGCCT CTTCATATTG GCGATCCTGT 150  
 TGTGCTCCCT GGCATTGGC AGTGTACAG TTGCACTCTT CTGAACCTGA 200  
 AGTCAGAATT CCTGAGAATA ATCCTGTGAA GTTGTCCCTGT GCCTACTCGG 250  
 GCTTTCTTC TCCCCGTGTG GAGTGGAAAGT TTGACCAAGG AGACACCACC 300  
 AGACTCGTTT GCTATAATAA CAAGATCACA GCTTCCTATG AGGACCGGGT 350  
 GACCTTCTTG CCAACTGGTA TCACCTCAA GTCCGTGACA CGGGAAAGACA 400  
 CTGGGACATA CACTTGTATG GTCTCTGAGG AAGGCGGCAA CAGCTATGGG 450  
 GAGGTCAAGG TCAAGCTCAT CGTGGTTGTG CCTCCATCCA AGCCTACAGT 500  
 TAACATCCCC TCCTCTGCCA CCATTGGAA CCGGGCAGTG CTGACATGCT 550  
 CAGAACAAAGA TGGTTCCCCA CCTTCTGAAT ACACCTGGTT CAAAGATGGG 600  
 ATAGTGATGC CTACGAATCC CAAAAGCACC CGTGCCTTCA GCAACTCTTC 650  
 CTATGTCCCTG AATCCCACAA CAGGAGAGCT GGTCTTGAT CCCCTGTCAG 700  
 CCTCTGATAC TGGAGAATAC AGCTGT 726

**FIG.\_4B**

consen02 SEQ ID NO:5

GCAGGGCAAAG TACCAGGGCC GCCTGCATGT GAGCCACAAG GTTCCAGGAG 50  
 ATGTATCCCT CCAATTGAGC ACCCTGGAGA TGGATGACCG GAGCCACTAC 100  
 ACGTGTGAAG TCACCTGGCA GACTCCTGAT GGCAACCAAG TCGTGAGAGA 150  
 TAAGATTACT GAGCTCCGTG TCCAGAAACT CTCTGTCTCC AAGCCCACAG 200  
 TGACAACTGG CAGCGGTTAT GGCTTCACGG TGCCCCAGGG AATGAGGATT 250  
 AGCCTTCAAT GCCAGGGTTC GGGGTTCTCC TCCCATCAGT TATATTTGGT 300  
 ATAAGCAACA GACTAATAAC CAGGGAACCC ATCAAAGTAG CAACCTAAG 350  
 TACCTTACTC TTCAAGCCTG CGGTGATAGC CGACTCAGGC TCCTATTCT 400  
 GCACTGCCAA GGGCCAGGTT GGCTCTGAGC AGCACAGCGA CATTGTGAAG 450  
 TTTGTGGTCA AAGACTCCTC AAAGCTACTC AAGACCAAGA CTGAGGCACC 500  
 TACAACCATG ACATACCCCT TGAAAGCAAC ATCTACAGTG AAGCAGTCCT 550  
 GGGACTGGAC CACTGACATG GATGGCTACC TTGGAGAGAC CAGTGCTGGG 600  
 CCAGGAAAGA GCCTGCCTGT CTTGCCATC ATCCTCATCA TCTCCTTGTG 650  
 CTGTATGGTG GTTTTACCA TGGCCTATAT CATGCTCTGT CGGAAGACAT 700  
 CCCAACAAAGA GCATGTCTAC GAAGCAGCCA GGGCACATGC CAGAGAGGCC 750  
 AACGACTCTG GAGAAACCAT GAGGGTGGCC ATCTTCGCAA GTGGCTGCTC 800  
 CAGTGATGAG CCAACTTCCC AGAATCTGGG GCAACAACTA CTCTGATGAG 850  
 CCCTGCATAG GACAGGAGTA CCAGATCATC GCCCAGATCA ATGGCAACTA 900  
 CGCCCGCTG CTGGACACAG TTCTCTGGA TTATGAGTTT CTGGCCACTG 950  
 AGGGCAAAAG TGTCTGTTAA AAATGCCCA TTAGGCCAGG ATCTGCTGAC 1000  
 ATAATTGCCT AGTCAGTCCT TGCCTTCTGC ATGGCCTTCT TCCCTGCTAC 1050  
 CTCTCTTCCT GGATAGCCCA AAGTGTCCGC CTACCAACAC TGGAGCCGCT 1100  
 GGGAGTCACT GGCTTGCCC TGGATTTCGC CAGATGCATC TCAAGTAAGC 1150  
 CAGCTGCTGG ATTTGGCTCT GGGCCCTCT AGTATCTCTG CCGGGGGCTT 1200  
 CTGGTACTCC TCTCTAAATA CCAGAGGGAA GATGCCATA GCACTAGGAC 1250  
 TTGGTCATCA TGCCTACAGA CACTATTCAA CTTGGCATC TTGCCACCAG 1300  
 AAGACCCGAG GGGAGGCTCA GCTCTGCCAG CTCAGAGGAC CAGCTATATC 1350  
 CAGGATCATT TCTCTTCCT CAGGGCCAGA CAGCTTTAA TTGAAATTGT 1400  
 TATTCACAG GCCAGGGTTC AGTTCTGCTC CTCCACTATA AGTCTAATGT 1450  
 TCTGACTCTC TCCTGGTGCT CAATAAATAT CTAATCATAA CAGCAAAAAA 1500  
 AAA 1503

**FIG.\_4C**

SEQ ID NO:11 CGAGTCCTT CGGGGCTGT TGTGTCACTG GCCTGATGCC GATGGGGACA AAGGGCAAG TCGAGAGGA ACTGTGTGC CTCTTCATAT 100  
 TGGCCTATCCT GTTGTGCTC CTGGCATTGG GCACTGTTAC AGTCAACTCT TCTGAACCTG AAGTCAGAAT TCTTGAGAAT AATCCCTGTA AGTGTGTCCTG 200  
 TGCCTACTCG GGCTTTCTT CTCCCCGTT GGAGTGGAG TTGAGCCAAG GAGACACCAC CAGACTCGTT TGCTTAAATA ACAAGATCAC AGCTTCCTAT 300  
 GAGGACCCGGG TGACCTTCTT GCCAACCTGGT ATCACCTCA AGTCCGTGAC AGCTGGACAT ACTGGGAGAC ACTGGGAGAC AGCTGGAT ACACCTGTAT GGTCTGTGAG GAAGGGGGCA 400  
 ACAGCTATGG GGAGGTCAAG GTCAAGCTCA TCGAGTCAAG TGGTCTGTGTT GCCTGCTGTT GCCTCTGCC ACCATGGGA ACCGGGAGCT 500  
 GCTGACATGTC TCGAGAACAG ATGGTCCCCC ACCTTCTGAA TACACTGGT TCAAAAGATGG GATAAGTGTG CCTACGAATC CCAAAGCAC CGGTGCTTC 600  
 AGCAACTCTT CCTATGTCCT GAATCCACA ACAGGAGGCC TGGTCTTGA TCCCCTGTCA GCCTCTGATA CTGGAGAATA CAGGTGTGAG GCACGGAAATG 700  
 GGTATGGAC ACCCATGACT TCAAATGCTG TCGGCATGGA AGCTGTGGAG CGGAATGTGG GGGTCATCGT GGCAGCCGTC CTTGTAACCC TGATTCTCCT 800  
 GGGAAATCTTG GTTTGGCA TCTGGTTGC CTATAGCCGA GGCCACTTGG ACAGAACAAA GAAAGGGACT TCGAGTAAGA AGGTGATTAA CAGCCAGCCT 900  
 AGTGCCTGAA GTGAAGGAGA ATTCAACAG ACCTCGTCAAT TCCCTGTGTG AGCCTGTG AGCTGTGTG GGTCAACGCC TATCATCTGC ATTGCTTA CTCAAGGTGCT 1000  
 ACCGGACTCT GGCCCCCTGAT GTCTGTAGTT TCAAGGATG CCTTACACC CCACAGGGCC CCTACTCTT TCGGATGTGT TTAAATAAT 1100  
 GTCAGCTATG TGCCCCATCC TCCTTCATGC CCTCCCTCCC TTTCCTACCA CTGCTGAGTG GCCTGGAACCT TGTTAAAGT GTTATTCCC CATTCTCTG 1200  
 AGGGATCAGG AGGAAATCCT GGGTATGCCA TTGACTTCCC TTCTAAGTAG ACAGCAAAAA TGGGGGGT CGCAGGAATC TGCACCTAAC TGCCCACCTG 1300  
 GCTGGCAGGG ATCTTGTAAAT AGCTTCTTG AGCTTGGTTC CCTGGCTCTT TGACGACCCAG GGCCAGCTGT TCTAGAGCGG GAATTAGAGG 1400  
 CTAGAGGGCC TGAATGGTT GTTGGTGT GACACTGGG TCCTTCATC TCTGGGGCC ACTCTCTCT GTCTTCCAT GGGAAAGTGCC ACTGGGATCC 1500  
 CTCTGCTG TCTTCCTGAA TACAAGCTGA CTGACATGAA CTGTGTGTG AGCTCTGT GTGAGAGCA TAGTAATTT TCAGAGAATCT 1600  
 TGAAGCCAA AGGATTAAA ACCGCTGCTC TAAAGAAAG AAAACTGGAG GTGGCTCAGG CCTGTAATCC CAGGGCTGA GGAGGGGA 1700  
 TCACCTGAGG TCGGGAGTTC ACCGCTGGCA TGGGATCAGCC TCAAGCTAACAT GGAGAAACCC TACTGGAAAT ACAAGTGTGAG CTGGTGTGCA 1800  
 AGCTGTCAG GAGGCTGGCA ACAAGAGCAA AACTCCAGCT CA 1842

FIG. - 5

SEQ ID NO:7

1 CCCCCCCCTC CGGGGACCGG TCCGGCCACG GGTCGGCCCA CGCGTCCGGG CCACAGAGG TTGAGCCTC TTGGTAGCA GGAGGCTGG AGAAAGGACA  
GGTGGCAG GGGGGCCC AGGGTCCC CCAAGGGCTT GGGAGGGG GGTGGTCTC AACCTGGAG AAACCATCGT CCTCCGACTT TCTTCCCTGT

101 GAAGTAGCTC TGGCTGTGAT GGGGATCTTA CTGGGGCTTC TACTCCTGGG GCACCTAACAA GTGGACACTT ATGGCCCTCC CATCCTGGAA GTGCCAGAGA  
CTTCATCGAG ACCGACACTA CCCCTAGAAT GACCCGGACG ATGAGGACCC CGTGATTTGT CACCTGTGAA TACCCGGAGG GTAGGACCTT CACGGTCTCT  
1 SEQ ID NO:2 M G I L L G L L G H L T V D T Y G R P I L E V P E S  
\*MET

201 CTGTAACAGG ACCTTGGAA GGGGATCTGA ATCTTCCCTG CACCTATGAC CCCCTGGCAAG GCTACACCCA AGTCTTGGCTG AACCTGGCTGG TACAACGTC  
CACATTGTCG TCGAACCTTT CCCCTACTT TAGAAGGGAC GTGGATACTG GGGGACGTTG CGATGTGGGT TCAGAACCCAC TTGACCGACC ATGTTGGCACC  
29 V T G P W K C D V N L P C T Y D P L Q G Y T Q V L V K W L V Q R G

301 CTCACCCCT GTCACCATCT TTCTTACGTGA CACCATATCC ACCAGGAAA CTACAGGCAAA CGTACGGGC CGCCCTGCATG TCAACCCACAA GGTTCCAGGA  
GAGTCTGGGA CAGTGGTACA AACGATGCACT GAGAAAGACCT CTGGCTATAGG TCCTCCGGTT CATGCTCCCG GGGGACGTPAC ACTCTGGTCTT CCAAGGTCT  
62 S D P V T I F L R D S S C D H I Q Q A K Y Q G R L H V S H K V P G

401 GATGATATCCC TCCAATTGAG CACCCCTGGAG ATGGATGACC GGACCCACTA CACGGTGTGAA GTCACCTGGC AGACTCTCTGA TGGCAACCAA GTCTGTGAGAC  
CTACATAGGG AGGTTAACCTC GTGGGACCTC TACCTACTGG CCTCTGGTGT GTCACACTT CAGTGGACCC TCTGAGGACT ACCGTTGGTT CAGGACTCTC  
95 D V S L Q L S T L E M D D R S H Y T C E V T W Q T P D G N Q V V R D

501 ATAAGATTAC TGAGCTCCCT GTCCAGGAAAC TCTCTGTCTC CAAGCCACA GTGACAACTG GCAGGGTTA TGGCTTCAAG GTGGCCCCAGG GAATGAGGAT  
TATTCTAATG ACTCGAGGCA CAGGTCTTG AGAGACAGAG GTTCGGGTGT CACTGTGTGAC CTCGGGGTCAAT ACCGAAGTGC CACGGGGTCC CTTACTCTA  
129 K I T E L R V Q K L S V S K P T V T T G S C Y G F T V P Q T V P G M R I

601 TAGCCTCAA TGGCAGGCTC GGGGTTCTCC TCCCATCAGT TATATTGGT ATAACCAACA GACTAATAAC CACGAACCA TCAAAAGTAGG AACCCCTAAGT  
ATCGGAAGTT ACGGTCCGAG CCCCAAGAGG AGGGTAGTCA ATATAAACCA TATTCTGGGT CTGATTATG GTCCCTGGGT AGTTTCATCG TTGGGATCA  
162 S L Q C Q A R G S P P I S Y I W Y K Q Q T N N Q E P I K V A T L S

FIG.-6A

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SEQ ID NO:7 701 ACCTTACTCT TCAAGCCGCC CCGTATAGCC CACTTACCCCT CCTATTCTG CACTGCCAAG GCGAACGGTTC CCTCTGAGCA GCACACCCAC ATCTGAACT  
TGGAAATAGA AGTTCGGAGC CCACTATCGG CTGAGTCCCGA GGATAAAGAC GTGACGGTTC CGGCTCCAC CGAGACTCTGT CGTGTGGCTG TAACACTTC  
SEQ ID NO:2 195 T L F K P A V I A D S G S Y F C T A K C Q V G S E Q H S D I V K F

801 TTGTGGTCAA AGACTCCCAA AGACCAAGAC TCAGGCCACCT ACAACCATGA CATAACCCCTT GAAAGCAACA TCTACAGTGA AGCAGTCCTG  
AACCCAGTT TCTGAGGAGT TTGGATGAGT TCTGGTACT GTGGTGGAA CTATGGGAA CTTTCGTTGT AGATGTCACT TCGTCAGGAC  
229 V V K D S S K L L K T K T E A P T T M T Y P L K A T S T V K Q S W

901 GGACTGGACC ACTGACATGG ATGGCTTACCT TGGAGACACC AGTCCCTGGCC CAGGAAAGAC CCTCCCTGTC TTTGCCATCA TCCTCATCAT CTCCCTGTC  
CCTGACCTGG TGACTGTACCC TACCGATGGA ACCTCTCTGG TCAACGCCCG GTCCTTCTC GGACGGACAG AACGGGTAGT AGGAGTAGTA GAGGAACACG  
262 D W T T D M D G Y L G E T S A G P G K S L P V F A I I L I I S L C

1001 TGTATGGTGC TTTTACCAT GGCTTATTC ATGCTCTCTGC CGAACAGAC CATCTCTACG AACCGGGACG GTAGAAACT CTCTCTCTT  
ACATACACC AAAATGTA CGGGATATAG TACGGAGAC CCTTCTCTAG CTACAGATGC TTGGTGGTC CTTCTTCA GAGGGAGAA  
295 C M V V F T M A Y I M L C R K T S Q Q E H V Y E A A R O

1101 CCATTTGA CCCCGTCCCT GCCCCTCAATT TTGATTAATG CGAGGAATG TGGAGAACCC AGACACCCAA TCCTAAGGGC GGAGGGCTTC  
GGTAAAAACT GGGCCAGGA CGGGAGTAA AACTAATGAC CGTCCTTTAC ACCTCCTTCC CCCAACACCG TGTCTGGTT AGGATTCGG CCTCCGGAGA

1201 AGGGTCAAGGA CATAGCTGCC TTCCCTCTCT CAGGCCACCTT CTGAGGTTGT TTGGCCCTC TGACACAAA CGATAATTAA GATCCATCTG CCTCTCTGCTT  
TCCCAGTCTT GTATGGACGG AAGGGAGAGA GTCCGGGAA GACTCCAACA AAACCGGAG ACTTGTGTT CCTATTAAAT CTAGGTAGAC GGAAGACGAA

1301 CCAGAATCCC TGGGGCTAG GATCCCTGATA ATTAAATGGC AAGAAATTGAG GGAGAGGGT GGGAAACAG GACCAAGGCC CCAAGTCCCT TCTTATGGGT  
GGTCTTGGG ACCCACCAC CTAGGACTAT TAATTAACCG TTCTTAACTC CGTCTTCCA CCCTTGGTC AGAAACCTAG AGGGGGCCA TCTTCCCTCC AGTGTATGAG  
CCACCGGAGA ACCCGGTATC CGGTGTACCC TCTCTCCCGT TCCTGAGACC TCTTGGTAC TCCCACCGT AGAAGCCGT AGAAGCCGT ACCGACGAGG TCACTACTCG

1401 GGTTGGCTCT TGGGCCATAG CGCACATGCC AGAGAGGCC ACCACTCTGG AGAGACCTAG TCTTCCCGT CGAGTACCC AGATCATGCC CCAGATCAAT GGCAACTACG CCCGGCTGGCT  
CTGAAAGGT CTTAGACCCG TTGGTGTAGA CACTACTCGG GACGTATGTA CGGTATCCCT GTCTCATGG TCTAGTGGC CGCTTACTTA CGCTTACTGA AGAATACCCAA

1501 CAACTCCCA GAATCTGGCC AACAACTACT CTGATGAGCC CTGCTATAGGA CAGGACTACCC AGATCATGCC CCAGATCAAT GGCAACTACG CCCGGCTGGCT  
CTGAAAGGT CTTAGACCCG TTGGTGTAGA CACTACTCGG GACGTATGTA CGGTATCCCT GTCTCATGG TCTAGTGGC CGCTTACTTA CGCTTACTGA AGAATACCCAA

SEQ ID NO:7

1601 GGACACAGT CCTCTGGATT ATGAGTTCTT CCCCACTGAG GGCAAAGTG TCTGTTAAA ATGCCCAT AGCCAGGAT CTGCTGACAT AATTGCCAT CCTGTGTCAA GAGACCTAA TACTAAAGA CCCGTCACTC CGGTTCAC AGACAAATTT TACGGGTTAA TCCGGTCTA GACGACTGTA TAAACGGGAT

1701 TCAGTCCCTG CCTCTGGCAT GGCCCTCTTC CCTGCTTACCT CTCTTCTCG ATAGCCCCAA GTGTCGGCTT ACCAACACTG GACCCGCTGG GAGTCAGTGG AGTCAGAAC GAAAGACGTA CGCGAAGAAG GGACGATGGA GAGAAGGACCC TATCGGTTT CACAGGGGA TGCTGTGAC CTCCGGGACC CTCACTGAC

1801 CTTGGCCCTG GAATTGGCA GATGCCATCTC AACTAAGCCA GCTGGCTGGAT TTGGCTCTGG CCCCTCTAG TATCTCTGCC GGGGGCTTCT GGTAATCTCTC GAAACGGGAC CTTAAACGGT CTACGTAGAG TTICATTGGT CGACGGACTA AACCGAGACC CGGGAAGATC ATAGAGACGG CCCCCGAAGA CCATGAGAG

1901 TCTAAATACC AGACGGAAAGA TCCCCATAGC ACTAGGACTT GGTCAATCATG CCTACAGACA CTATTCAACT TTGGCATCTT GCCACCAAGA GACCCGAGGG AGATTTATGG TCTCCCTCTT ACGGCTATCG TGTATCTGAA CCAGTAGTAC CGATGTCTGT GATAAGTTGA AACCGTAGAA CGGTGGTCTT CTGGGCTCCC

2001 AGGCTCAGCT CGGCCAGCTC AGAGGACCAAG CTATATCCAG GATCATTTCT CTTCTTCAG GCCCAGACAG CTTTTAATTG AATTCTTAT TTACAGGGCC TCCGAGTCGA GACGGTGGAG TCTCCTGGTC GATATGGTC CTAGTAAGA GAANGAGTC CGGTCTGTC GAAATTAAC TTAAACATA AAGTGTCCC

2101 AGGGTTCACT TCTGCTCCTC CACTATAAGT CTATATGTTCT GACTCTCTCC TGGTGTCTAA TAAATATCTA ATCATACAG C TCCCAAGTCAGCA AGACGGGGAG GTGATTTCA GATTACAGCA CTGAGAGGG ACCACGGAGTT ATTTATAGTT TACTATTCCTC G

**FIG.-6C**

SEQ ID NO:8

CCCAGAAGTTCAAGGGCCCCGGCCTCCTGCGCTCCTGCCGCCGGGACCCCTGACCTCCT  
 CAGAGCAGCCGGCTGCCGCCCGGGAAAGATGGCGAGCAGGAGGCCACCGCCTCCTCCT  
 GCTGCTGCTGCGCTACCTGGTGGTCGCCCTGGGCTATCATAAGGCCTATGGGTTTCTGC  
 CCCAAAAGACCAACAAGTAGTCACAGCAGTAGAGTACCAAGAGGGCTATTTAGCCTGCAA  
 AACCCCAAAGAAGACTGTTCCCTCAGATTAGAGTGGAAAGAAACTGGTCGGAGTGTCTC  
 CTTGTCTACTATCAACAGACTCTCAAGGTGATTTAAAAATCGAGCTGAGATGATAGA  
 TTTCAATATCCGGATCAAAATGTGACAAGAAGTGTGCGGGAAATATCGTTGTGAAGT  
 TAGTGCCCCATCTGAGCAAGGCCAAACCTGGAAGAGGATACAGTCACTCTGGAAGTATT  
 AGTGGCTCCAGCAGTTCCATCATGTGAAGTACCCCTCTGCTCTGAGTGGAACTGTGGT  
 AGAGCTACGATGTCAAGACAAAGAAGGGAATCCAGCTCCTGAATAACACATGGTTAAGGA  
 TGGCATCCGTTGCTAGAAAATCCCAGACTGGCTCCAAAGCACCAACAGCTCATACAC  
 AATGAATACAAAAACTGGAACTCTGCAATTAAACTGTTCAAACGGACACTGGAGA  
 ATATTCCCTGTGAAGGCCGCAATTCTGTTGGATATCGCAGGTGTCCTGGAAACGAATGCA  
 AGTAGATGATCTCAACATAAGTGGCATCATAGCAGCCGTAGTAGTTGTGGCCTAGTGAT  
 TTCCGTTGTGGCCTGGTGTATGCTATGCTCAGAGGAAAGGCTACTTTCAAAGAAC  
 CTCCTCCAGAAGAGTAATTCTCATCTAAAGCCACGACAATGAGTAAAATGTGAGTG  
 GCTCACGCCTGTAATCCCAGCACTTGGAAAGGCCGGCGGGCGGATCACGAGGTAGGA  
 GTTCTAGACCAAGTCTGCCAATATGGTGAACCCCCATCTACTAAATACAAAAATTAG  
 CTGGGCATGGTGGCATGTGCCTGCAGTTCCAGCTGCTGGGAGACAGGAGAATCACTGA  
 ACCCGGGAGGCGGAGGTTGCAGTGAGCTGAGATCACGCCACTGCAGTCCAGCCTGGTAA  
 CAGAGCAAGATTCCATCTAAAAATAAAATAAAATAAAATAACTGGTTTACCTGATATTG  
 TGTAGAATTCTTACAATAATAGCTTGTATATTG

**FIG.\_7**

SEQ ID NO:9

MARRSRHRLLLLLRLYLVALGYHKAYGFSAPKDQQVVTAVEYQEAILACKTPKKT  
 VSSRLEWKKLGRSVSFVYYQQTLQGDFKNRAEMIDFNIRIKNVTRSDAGKYRCEVSAP  
 SEQQNLEEDTVTLEVLVAPAVPSCEVPSSALSGTVVELRCQDKEGNPAPEYTWF  
 KDGIRLLENPRLGSQSTNSTSYTMNTKTGTLQFNTVSKLDTGEYSCEARNSVG  
 YRRCPGKRMQVDDLNISGIIAVVVVALVISVCGLGVCYAQRKGYFSKETSF  
 QKSNSSSKATTMSENVQWLTPVIPALWKAAAGGSRGQEF

**FIG.\_11**

SEQ ID NO:5

1 CGAGGAAAG TACCAAGGGCC GCTCTCCATCT GACCCACAG CTTCCACAG ATGTATCCCT CCAATTGAGC ACCTGGCC TGGATGACCG GACCCACTAC  
 CGTCGGTTTC ATGGTCCCGG CGGACGTACA CTGGGTGTTCA CTGGACCTCT TACATAGGGA CGTTAUCCTCG GGGACCTCT ACCTACTGGC CTCGGGTATG  
 ^42257. f1 SEQ ID NO:18 ^42257. p1 SEQ ID NO:22

101 ACGTGTGAG TGACCTGGCA GACTCTCTAT GGCACCAAG TCCTGAGAGA TACGATTACT GAGCTCGTG TCCAGAAACT CTCTGCTCC AAACCCACAG  
TGACACATTC ACTGGGCCCC CTGGGGACTA CGCTGGGACTA CGCTGGGTTTC AGGACTCTCT ATTCTTAATGA CTGGCTTGA AGGCTTCC GGGAGG TTCGGGTGTC

201 TGACAACTGC CAGGGTTAT GGCCTCACCG TGGCCCAAGG ATAGGAGGTT AGCCTTCAAT CCCAGGCTTC CGGAGGCTTC GGGAGG TCCCATCACT TATATTGCT  
ACTGGTACCC GTCGCCATA CGGAAGTGGCC ACGGGGTCCC TTACTCCTAA TCGGAAGTTA CGGAGGAGG CCCAAAGGAG AGGGTAGCTCA ATATAAACCA

301 ATAAGCAACA GACTATAAC CAGGGAAACCC ATCAAAGTAG CAACCTTAAG TACCTTACTC TTCAAGCCTG CGGTGATAGC CGACTCAGGC TCCTTATTCT  
TATTGGTTCT CTGATTATTG GTCCCCCTGGG TAGTTTCATC GTTGGGATTTC ATGGAATGAG AAGTCCGAC GGCACTATCG GCTGACTCCG AGGATAAAGA

401 GCACTGCCAA GGCCCAAGCTT GGCTCTGAGC ACCACACCGA CATTGCAAG TTTGTGAGC AAAGACTCTC AAAGTACTCT AAGACCAAGA CTGAGGGACC  
CCTGACGGTT CCCCCTCAA CCGAGACTCC CTGCTCTCC CTAACACTTC AMACCAAGT TTTGTGAGG TTTCGATGAG TTCCTGTTCT GACTCCCTGG  
 ^42257. f1 SEQ ID NO:20

501 TACAAACATG ACATACCCCT TGAAGGCAAC ATCTACAGTG AAGCAGTCCT GGGACTGGAC CACTGACATG GATGGCTACC TTGGAGAGAC CAGTCCCTGGG  
ATGTTGGTAC TGTATGGGA ACTTTGGTT TAGATGTCAC TTGTCAGGA CCTGACCTG GTGACTGTAC CTACCGATGG AACCTCTCTG GTCACGGACCC

601 CCAGGAAGA GCCTGCTGT CTGGCCATC ATCCTCATCA TCTCTTGTG CTGCTATGGC GTGGCTTACCA TGGCCTATAT CATGGCTCTGT CGGAAGACAT  
GCTCTTTCT CGGACGGACA GAAACGGTAG TAGGAGTAGT AGAGGAACAC GACATACCAAC CAAAATGGT ACCGGATATA GTACGAGACA GCCTCTGT  
 ^42257. f2 SEQ ID NO:19

701 CCCACAGA GCATGCTAC GAAGCAGCCA GGGCACATGC CAGAGGGCC AACGACTCTG GACAAACCAT GAGGGTGGCC ATCTTGGAA GTGGCTGCTC  
CGGTGTTCT CGTACAGTG CTGGCTGGGT CCCGTGTACG GTCTCTCCGG TGCTTGGTA CTGGTGGAC CTCTTGGTA CTGGTGGAG  
 TAGAAGGGTT CACCGACAG

**FIG.\_ 9A**

SEQ ID NO:5

801 CAGTGTAG CCAACTTCCC AGAATCTGGG CCACCAACTA CTCTGTAG CCCTGCATAG GACAGGAGTA CCAGATCATC GCCCAGATCA ATGGCAACTA  
GTCACACTC GGTGAAAGG TCTTAGACCC CGTGTGTGAT GAGACTACTC CGGACTATC CTGTCCTCAT GGTCTAGTAG CGGCTCTAGT TACCGGTGTGAT

901 CGCCCCCTG CTGGCACACAG TTCCCTCTGGA TTATGAGTTT CTGGCCACTG AGGGCAAAAG TGCTGTTAA AAATCCCCA TTAGGCCAGG ATCTGCTGAC  
GGGGGGGAC GACCTGTGTC AAGGAGACCT AATACTCAA GACCGGTGAC TCCGGTTTC AGACAAATT TTACGGGT ATCCGGTCC TAGACGACTG

1001 ATAATGCCCT AGTCAGTCTCT TGCCCTCTGC ATGGCCCTTCT CTCCTGCTAC CTCTCTCCCT GGTAGGCCA AAGTCGCC 3TACCAACAC TGAGGCCGCT  
TATTACCGA TCACTCAGGA ACGGAAGACG TACCGGAAGA AGGGACGATG GAGGAAGGA CCTATCGGGT TTACACGGG GATGGGTCTG ACCTCGGGCA

1101 GGGACTCACT GCGCTTGCCC TGGAAATTCC CAGATGCATC TCAAGTAAGC CAGCTGCTGG ATTGGCTCT GGGCCCTCT AGTATCTCTG CCGGGGCTT  
CCCTCACTGA CGGAAACGG ACCTTAACG GTCTACGTAG AGTCATTCC GTCCGCGACC TAACCGAGA TCATAGAGAC GGGCCCCGAA  
~42257.f2 SEQ ID NO:21

1201 CTGGTACTCC TCTCTAAATA CCAGAGGGAA GATGCCATA GCACTAGGAC TTGGTCTCATCA TGCCTACAGA CACTATCAA CTTGGCATC TTGGCACCG  
GACCATGAGG AGAGATTAT GGTCTCCCTT CTACGGGTAT CGTGATCTG AACCAGTACT ACCGATGTCT GTGATAAGTT GAAACCGTAG AACGGGGTC

1301 AAGACCCGAG GGGAGGCTCA CCTCTGCCAG CTCAGAGGAC CAGCTATAC CAGGATCATC TTCTCTCTT CAGGGCAGA CAGCTTTAA TTGAAATTG  
TTCTGGCTC CCCTCCGAGT CGAGACGGTC GAGTCTCCTG GTCGATATAG GTCGATATAAG GAGAAAGAA GTCCGGGTCT GTGAAATT AACTTAACAA

1401 TATTCACAG CCAGGGTTC AGTTCTGCTC CTCACATCA AGTCTAAATCT TCTGACTCTC TCTCTCTGCTT CAAATCATAA CAGCAAA  
ATAAAGTGTGTC CGGTCCCAAG TCAAGACCGAG GAGGTGATAT TCAGATTACA AGACTGAGAG AGGACACGA GTTAAATTATA GATTAGTATT GTCGTTTTT

1501 AAA  
TTT

FIG.- 9B

A33 HUMAN A33 ANTIGEN PRECURSOR - HOMO SAPIENS

A33\_HUMAN - A33 ANTIGEN PRECURSOR - HOMO SAPIENS (319 aa)  
SCORE = 246 (86.6 BITS), EXPECT = 2.8e-19, P = 2.8e-19  
IDENTITIES = 81/268 (30%), POSITIVES = 131/268 (48%), AT 121,17, FRAME = +1

SEQ ID NO:23	121	LALGSVTVHSSEPEVRIPENNPKLSCAYSGFSSPR--V EW-KFDQGDDTRLVC--YNN
SEQ ID NO:24	17	VTVDAAISVETPQDVLRASQGKSVTLPCTYHTSTSREGLIQWDKULLTHTERVV IWPPFSN

DNA40628	283	K--ITAS-YEDRVTFL-----PTGIFKSVTREDTGTYTCMVS---EEGGNSYGEVKVK
		* * + . * .
A33	human	77 KNYIHGELYKNRVSISNNAEQSDASITIDQLTMADNGTYECVSLSMSDLEGNT-KSVR

SSYVLNPTTGEILV	607	SSYVLNPTTGEILV - FDPLSASDTGEYSCEARNNGYGTPTMSNAVRMEAVERNVGV -- IVA
LAQPASQFVSLKNISTDTGGYYICTSSNEEGTQFCNITAVRSPSMNVALYVGIAV	187	LAQPASQFVSLKNISTDTGGYYICTSSNEEGTQFCNITAVRSPSMNVALYVGIAV

DN4A0628	775	AVLVTLLILGILVFGIWFAYSRGHFDFRT--KKGTSSKKVITYSQP
	*	* * . * * . . .
A33	244	GUYAALIILIGIILIX---CCCCRGKDDNTEDKEDARPNEAYEEP
human		

FIG. 10A

SCORE = 245 (86.2 BITS), EXPECT = 3.6e-19, P = 3.6e-19  
IDENTITIES = 83/273 (30%), POSITIVES = 131/273 (47%), AT 112,12, FRAME = +1

DNA4 0628	112	LCSL--ALGSVTVHSSEPEVRIPENNPKVLSAYSGFSSPR--	VEW-KFDQGDTTRLVC
SEQ ID NO:25		**.: . . . * . . . * . . . * . . . * . . . * . . . * . . . * . . . * . . . *	
A33 human	12	LCAVRVTVDAAISVETPQDVLRASQGKSVTLPCYHTSTSSREGLIQWDKLLTHTERVVI	
SEQ ID NO:26			

DNA4 0628 274 --YNNK-- ITAS - YEDRVTFL - - - - PTGITEFKSVTREDTGTYTCMVSEEGGNSYGEVK  
 A33 \_human 72 WPFNSKNYIHGELYKNRVSISNNAEQSDASITIDQLTMADNGTYECSVSLMS - DLEGNTK

DNA4 0628	421	--VKLIVLVPPSKPTVNIPSSATIGNRAWLT	TCSEQDGSSPPSEYTWFKDGIVMPTNPKSTR
		* . * . * . * . * . *	* . * . * . * . *
A33	human	131	SRVRLLVLPVPPSKPECGIEGETIIGNNIQLTCQSKEGSPTPQYSWKRYNILNQEOP----

DNA4 0628	595	AFNSSSYVLNPTTGEV - FDPLSASDTGEYSCEARNGTPTMSNAVRMEAVERNVGV--
	.	* * . * . * . * . * . * . * . * . * . * . * . * . * . * . * . * .
A33 human	187	-----LAQPASGQPVSLKNISTDTSGYYICTSSNEEGTQFCNITAVRSPSMVALYV

DNA4 0628	766	-IVAAVLVTILLGILVFGIWFAYSRGHFDRT-	-KKGTSSKKVIVSQP
	*	**.**.**.**.**.**.**.**.**.**.**.**.	**.**.**.**.**.**.**.**.**.**.**.**.
A33 human	240	GIAVGVVAALIIIGIIY--	CCCCRGKDDNTEDKEDARPNRAYEEP

FIG. 10B

SEQIDNO: 6 A33\_hum 1 ..... M V G K W W P V L W T L C A V R V T V D A I S V E T P O O V L R A S O G K S V T L  
 SEQIDNO: 1 40628 1 W G T K A Q V E R K L L C I L F I L A I L L C S . . L A L G S V T V H S S E P E V R I P E N N P V K L

A33\_hum 42 P C T Y H T S T S R E G L I O W D K L L T H T E R V Y I W P P F S N K N Y I H G E L Y K N R V S I  
 40628 49 S C A Y S G F S S P R . . V E W . K F D Q G D T T R L Y C . . Y N N K . . I T A S . Y E D R V T F

A33\_hum 92 S N N A E Q S D A S I T I D O L T M A D N G T Y E C S V S L W S D L E G N T K S R V A R L L V L V P P  
 40628 90 . . . . . L P T G I T F K S V T R A E D T G T Y T C M V S E E G G . N S Y G E V K V K L I L V L V P P

A33\_hum 142 S K P E C G I E G E T I I G N N I Q I L T C O S K E G S P T P Q Y S W K R Y N I L N O E O P . . . . .  
 40628 133 S K P T V N I P S S A T I G N R A V L T C S E Q D G S P P S E Y T W F K D G I U V M P T N P K S T R A

A33\_hum 187 . . . . . L A Q P A S G Q P V S L K N I S T D T S G Y I C T S S N E E G T Q F C N I T V A V R S  
 40628 183 F S N S S Y V L N P T T G E . L V F D P L S A S D T G E Y S C E A R N G Y G T P W T S N A V R W E A

A33\_hum 231 P S M N V A L Y V G I A V G V V A A L I I G I I I Y C C . C C R G K D D N T E D K E D A R P N R E  
 40628 232 V E R N V G V . . . I V A A V L V T I L L G I L V F G I W F A Y S R A G H F D R T K G T S S K K V

A33\_hum 280 A Y E E P P E Q L R E L S R E R E E D D Y R Q E E Q R S T G R E S P D H L D Q  
 40628 279 I Y S O P S A R S E G E F K O T S S F L V

SEQ ID NO: 6 A33\_hum 1 M V G K M W P V [WTLCAVRVTVD AIS V E T P A D V L R A S Q G K S V T L P C T Y H T S T S  
SEQ ID NO: 2 45416 1 . M G I L L G L L L G H L T V D T Y G R P I L E V P E S Y T G P W K G . D V N L P C T Y D P L Q G

A33\_hum 51 S R E G L I Q W D K [L L T H T E R V V [W . P F S N K N Y I H G E L Y K N R V S I S N N A E Q S D  
45416 49 Y T Q V L V K W . . L Y Q R G S D P V T I F L R D S S S G D H I Q Q A K Y Q G R L H V S H K V . P G D

A33\_hum 100 A S I T I D Q L T M A D N G T Y E C S Y S . L M S D L E G N T K S A V . . . . . A L L V L V P P S  
45416 96 V S L Q A L S T L E M D D A R S H Y T C E V T W Q T P D G N Q V V R D K I T E L R V Q K L S V S K P T V

A33\_hum 143 K P E C G I E G E T I I G N N I Q L T C O S K E G S P T P Q Y S W K R Y N I L N O E Q P L A O P A S  
45416 146 T T G S G Y G F T V P Q G W R A I S L O C A A R . G S P P I S Y . W . Y K O O T N N Q E P I K V A T

A33\_hum 193 G Q P V S L K N I S T D T S G Y Y I C T S S N E E G T . Q F C N I . T V A V R S P S H N V A L Y V G  
45416 193 L S T L L F K P A V I A D S G S Y F C T A K G Q V G S E Q H S D I V K F V V K D S S K L L K T K T E

A33\_hum 241 I A V G V V A A [ I I G I I I Y C C C C A R G K D D N T E D K E D A R P N R E A Y E E P P E Q L R E  
45416 243 A P T T M T Y P L K A T S T V K O S W D W T T D M D G Y L G E T S A G P G K S L P V F A I I I S

A33\_hum 291 L S R E R E E E D D Y R O E E Q R S T G R E S P D H L D Q  
45416 293 L C C W V V F T M A Y I H L C R K T S Q Q E H V Y E A A R

SEQ ID NO: 6 A33\_hum 1 . . . M V G K M W P V L W T L C A V R V T V D . . . . A I S V E T P O D V L R A S Q G K S V T L P C  
 SEQ ID NO: 9 35638 1 M A R R S R H R L L L L R Y L V V A L G Y H K A Y G F S A P K D O o a y v t a v e y o e a i l a c

A33\_hum 44 T Y H T S T S S R E G L I Q W D K I L L T H T E R V Y I W P F S N K N Y I H G E L Y K N R V S I S N  
 35638 51 . . K T P K K T V S S R L E W K K L . . . . G R S Y S F V Y Y Q Q T . L Q G D . F K N R . . . .

A33\_hum 94 N A E Q S D A S I T I D Q L T W A D N G T Y E C S Y S L M S D L E G N . T K S A V Y A R L L V L Y P P S  
 35638 87 . A E N I D F N I R I K N Y I R S D A G K Y R C E V Y S A P S E Q G Q N L E E D T V T L E V L V A P A

A33\_hum 143 K P E C G I E G E T I I G N N I Q L T C Q S K E G S P T P Q Y S W K A Y N I L N Q E Q P L A Q P A S  
 35638 136 V P S C E V P S S A L S G T V V E L R A C Q D E G N P A P E Y T W F K D G I A L L E N P R L G S O S

A33\_hum 193 G Q P V S L K N I S T D T S G Y Y I C T S S N E E G T O F C N I T V A V . . . R S P S M N V A L Y V  
 35638 186 T N S S Y T M N T K T G T L O F N T . V S K L D T G E Y S C E A R N S V G Y R A C P G K R M Q V D D

A33\_hum 240 G I A V G V V A A L I I G I I I Y C C . . . C C R A G K D D N T E D K E D A R P N R E A Y E E P P E  
 35638 235 L N I S G I I A A V V V A L V I S V C G L G V C Y A Q R K G Y F S K E T S F Q K S N S S S K A T T

A33\_hum 287 Q L R E L S A . E R E E E D D Y R Q E E Q R S T G R E E S P D H L D Q  
 35638 285 W S E N V Q W L T P V I P A L W K A A A G G S R G Q E F

SEQ ID NO:10 jam 1 **W G T E G K A G R K L L F L F T - S M W I L C S L V A G K G S V Y T A a S D V Q V P E N E S I K L I C**  
 SEQ ID NO:1 40628 1 **W G T X A Q V E R K L L C F I L A I L L C S L A L G S V T Y H S S E P E V R I P E N N P V K L S C**

jam 50 **T Y S G F S S P R A V E W K F V Q G S T T A L V C Y N S Q I T A P Y A D R V T F S S S G I T F S S V T**  
 40628 51 **A Y S G F S S P R A V E W K F D Q G D T T A L V C Y N N K I T A S Y E D D R V T F L P T G I T F K S V T**

jam 100 **R K D N G E Y T C H V S E E G G O N Y G E V S I H I T V L V P P S K P T I S V P S S V T I G N R A V**  
 40628 101 **R E D T G I Y T C H V S E E G G N S Y G E V K V K L I V L V P P S K P T V N I P S S A T I G N R A V**

jam 150 **L T C S E H D G S P P S E Y S W F K D G I S H L T A D A K K T R A F W N S S F T I D P K S G D L I F**  
 40628 151 **L T C S E A D G S P P S E Y T W F K D G I . V M P T N P K S T R A F S N S S Y V L N P T T G E L V F**

jam 200 **D P V T A F D S G E Y Y C O A N G Y G T A A M R S E A A H M D A V E L N V G G I V A A V L V T L I L**  
 40628 200 **D P L S A S D T G E Y S C E A R N G Y G T P M T S N A V R M E A V E R N V G G I V A A V L V T L I L**

jam 250 **L G L L I F G V W F A Y S R G Y F E T T K K G T A P G K K V I Y S Q P S T R S E G E F K Q T S S F L**  
 40628 250 **L G I L V F G I W F A Y S R G H F D R T K K G T . S S K K V I Y S Q P S A R S E G E F K Q T S S F L**

jam 300 **V**  
 40628 299 **V**

SEQ ID NO: 10 jam 1 M G T E G K A G R K L L F L F T S M I L G S L . V O G K G . S V Y T A Q S D V O V P E N E S I K L T  
SEQ ID NO: 2 45416 1 . . . . . M G I L L G L L L G H L T Y G A P I L E V P E S V T G P W K G D V N L P

jam 49 C T Y S . . . G F S S P R V E W K F V Q G S T T A L V . . . C Y N S C I . T A P Y A D R V T F S .  
45416 41 C T Y D P L O G Y T Q V L V K W L V Q R G S O P V T I F L R D S S G D H I Q Q A K Y Q G R L H V S H

jam 90 . . . . S S G I T F S S V T R K D N G E Y T C M Y . . . S E E G G O N Y G E V S I H L T Y L . V P P .  
45416 91 K V P G D V S L Q L S T I E M D D O R S H Y T C E V T W Q T P D G N Q V V R D K I T E L R A Y Q K L S V

jam 132 S K P T I S V P S . . . S V T I G N R A Y L T C S E H D G S P P S E Y S W F K D G I S H M L T A D A  
45416 141 S K P T V T T G S G Y G F T V P Q G M A I S L O C A R . G S P P I S Y I W Y K O O T N . . N Q E P

jam 178 K K T R A F W N S S F T I D P K S G D L I F D P V T A F D S G E Y Y C O A Q N G Y C T A M R S E A A  
45416 188 I K V A T L . . . . . . . . . . . . S T L L F K P A V I A D S G S Y F C T A K G O V G S E Q H S D I V

jam 228 H . . . M D A V E L N V G G I V A A V L V T I L G L L I F G . . . V W F A Y S R G Y F E T T K K  
45416 227 K F V V K D S S K L L K T K T E A P T T M T Y P L K A T S T V K O S W D W T T O M D G Y L G E T S A

jam 272 G T A P G K K V I Y S Q P S T R S E G E F K O T S S F L V  
45416 277 G P G K S L P V F A I I I S L C C M V V F I W A Y I W L C R K T I S Q Q E H V Y E A A R

**FIG. - 16**

SEQ ID NO: 10	jam	1	W G T E G K A G R K L L F T S M I L G S L V O G K G S V Y T A o s D v o v . . . P E N E S I K L
SEQ ID NO: 29	35638	1	• • M A R R S R H A R L L L R Y L V V A L G Y H K A Y G F S A P K C o o v t a v e y Q E A I L
jam	48	T C . T Y S G F S S P R Y E W K F V Q G S I T A L V C Y N S Q I T A P Y A D R V T F S S S G I T F S	
35638	49	A C X T P K K T V S S R L E W K K L . G R S V S F V Y Y Q Q T L O G D F K N R A E M I D F N I R I K	
jam	97	S Y T R K D N G E Y T C M V S . . E E G G A N Y G E V S I H T V L V P P S S K P T I S V P S S V T I	
35638	98	N Y T R S D A G K Y R C E Y S A P S E Q A N L E E D T V T L E V L V A P A V P S C E V P S S A L S	
jam	145	G N R A V L T C S E H D G S P P S E Y S W F K D G I S M L T A D A K K T R A F M N S S F T I D P K S	
35638	148	G T V V E L R C Q D K E G N P A P E Y T W F K D G I R L L . E N P R I G S O S T N S S Y T M N T K T	
jam	195	G D L I F D P V T A F D S G E Y Y C O A Q N G Y G T A M A S E A A H W D A V E L N V G G I V A A V L	
35638	197	G T L O F N T V S K L D T G E Y S C E A R N S V G . Y R R C P G K R M Q V D D L N I S G I I A V V	
jam	245	V T L I L L G L L I F G V W F A Y S R G Y F E T T K G T A P G K K V I Y S O P S T R S E G E F K Q	
35638	246	V V A L V I S V C G L G V C Y A Q R K G Y F . . . S K E T S F O K S N S S S K A T I M S E N V Q O W L	
jam	295	T S S F L V	
35638	293	T P V I P A L W K A A G G S R G Q E F	

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FIG.-17

SEQ ID NO: 6 A33\_hum 1 . . . . . **W V G K M W P V L W T** . L C A V R V T V D A I S V E T P Q D V L R A S O G K S V T L P C T  
SEQ ID NO: 10 jam 1 **W G T E G K A G R K L L F L F T S M I L G S L V Q G K G S V Y T A Q** S D V Q V P E N E S I K L T C T

A33\_hum 45 **Y H T S T S S R E G L I Q W D K L L T H T E R V V I W P F S N K N Y I H G E L Y K N R V S I S N N**  
jam 51 **Y S G F S S P R** . . . V E W . K F V Q G S T T A L V C . . Y N S Q . . I T A P . Y A D R V T F S S .

A33\_hum 95 **A E Q S D A S I T I D Q L T W A D N G T Y E C S Y S L W S D O L E G N T K S R V R L L** V L V P P S K P  
jam 91 . . . . S G I T F S S V T R K D N G E Y T C M V S E E G G . Q N Y G E V S I H L T V L V P P S K P

A33\_hum 145 E C G I E G E T I I G N N I Q L T C O S K E G S P T P Q Y S W K R Y N I I N Q E Q P L A Q P A S G Q  
jam 135 T I S V P S S V T I G N R A V L T C S E H D G S P P S E Y S W F K D G I S M I L T A D A K K T R A F M

A33\_hum 195 P V S L K N I S T D T S G Y Y I C T S S N E E G T O F C N . . . . I T V A V R S P S H N . . . V A L  
jam 185 N S S F T I D P K S G D L I F D P V T A F D S G E Y Y C Q A Q N G Y G T A W R S E A A H M D A V E L

A33\_hum 238 Y V . G I A V G V V A A L I I G I I Y C . . . C C C R G K D D N T E D K E D A R P N R E A Y E E  
jam 235 N V G G I V A A V L V T L I I L G L L I F G V W F A Y S R G Y F E . I T K K G T A P G K X V I Y S Q

A33\_hum 284 P P E Q L R E R E E E D D Y R Q E E Q R S T G R E S P D H L D Q  
jam 284 P S T R S E G E F K Q T S S F L V

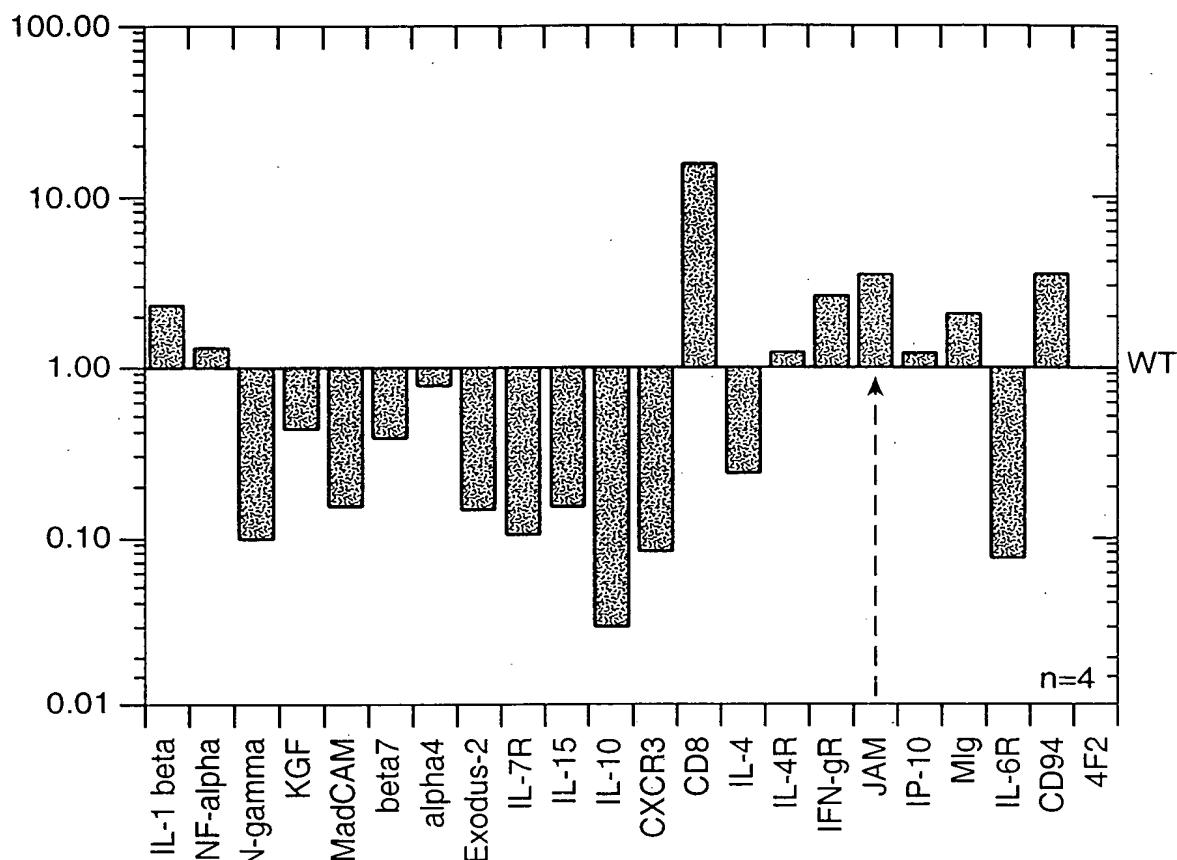
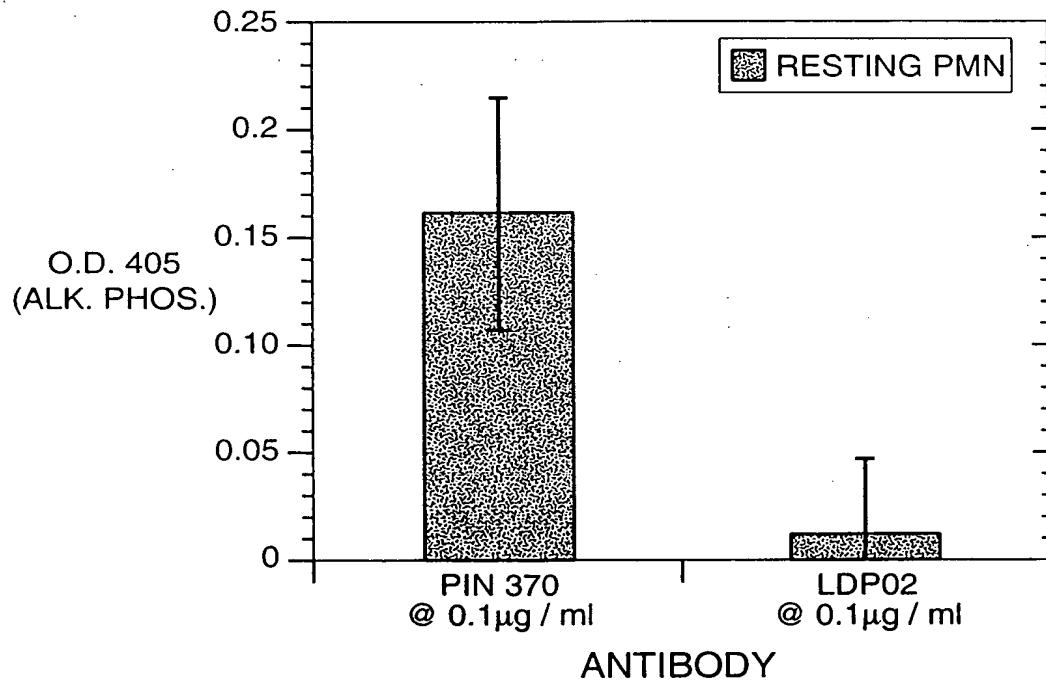
**FIG..18**

<u>TISSUE</u>	<u>EXPRESSION</u>	<u>TISSUE</u>	<u>EXPRESSION</u>	<u>TISSUE</u>	<u>EXPRESSION</u>
WHOLE BRAIN	+	HEART	++	KIDNEY	+++
AMYGDALA	+	AORTA	+	LIVER	++
CAUDATE NUCLEUS	+	SKELETAL MUSCLE	+	SMALL INTESTINE	++
CEREBELLUM	-	COLON	+++	SPLEEN	++
CEREBRAL CORTEX	+	BLADDER	++	THYMUS	++
FRONTAL LOBE	+	UTERUS	+	PERIPHERAL LEUKOCYTE	+
HIPPOCAMPUS	+	PROSTATE	+++	LYMPH NODE	+
MEDULLA OBLONGATA	+	STOMACH	+++	BONE MARROW	+
OCCIPITAL LOBE	+	TESTIS	++		
PUTAMEN	+	OVARY	++	APPENDIX	+
SUSTANTIA NIGRA	+	PANCREAS	++	LUNG	++++
TEMPORAL LOBE	+	PITUITARY GLAND	++	TRACHEA	+++
THALAMUS	+	ADRENAL GLAND	++	PLACENTA	++++
NUCLEUS ACCUMBENS	+	THYROID GLAND	++		
SPINAL CORD	-	SALIVARY GLAND	++	FETAL BRAIN	+
		MAMMARY GLAND	++	FETAL HEART	+
				FETAL KIDNEY	++
				FETAL LIVER	+++
				FETAL SPLEEN	+
				FETAL LUNG	++++

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FIG.\_19

RELATIVE EXPRESSION

**FIG.\_20****FIG.\_21**